

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Human Melanocyte stimulating hormone receptor

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/387,805
(B) FILING DATE: 21-FEB-95
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/DK93/00273
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(B) FILING DATE: 21-AUG-92

(ix) PRIOR APPLICATION DATA:

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(B) FILING DATE: 10-SEP-92

(x) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: DK 0528/93
(B) FILING DATE: 05-MAY-93

(xi) ATTORNEY/AGENT INFORMATION:

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 (C) REFERENCE/DOCKET NUMBER: 1102.0160000

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 169..1122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGAGAGGGTG	TGAGGGCAGA	TCTGGGGGTG	CCCAGATGGA	AGGAGGCAGG	CATGGGGAC	60
ACCCAAGGCC	CCCTGGCAGC	ACCATGAACT	AAGCAGGACA	CCTGGAGGGG	AAGAACTGTG	120
GGGACCTGGA	GGCCTCCAAC	GACTCCTTCC	TGCTTCCTGG	ACAGGACT	ATG GCT GTG	177
				Met	Ala Val	
				1		
CAG GGA TCC CAG AGA AGA	CTT CTG GGC TCC CTC AAC TCC ACC CCC ACA					225
Gln Gly Ser Gln Arg Arg	Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr					
5	10	15				
GCC ATC CCC CAG CTG GGG CTG GCT GCC AAC CAG ACA GGA GCC CGG TGC						273
Ala Ile Pro Gln Leu Gly Leu Ala Asn Gln Thr Gly Ala Arg Cys						
20	25	30	35			
CTG GAG GTG TCC ATC TCT GAC GGG CTC TTC CTC AGC CTG GGG CTG GTG						321
Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu Gly Leu Val						
40	45	50				
AGC TTG GTG GAG AAC GCG CTG GTG GTG GCC ACC ATC GCC AAG AAC CGG						369
Ser Leu Val Glu Asn Ala Leu Val Ala Thr Ile Ala Lys Asn Arg						
55	60	65				
AAC CTG CAC TCA CCC ATG TAC TGC TTC ATC TGC TGC CTG GCC TTG TCG						417
Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu Ala Leu Ser						
70	75	80				
GAC CTG CTG GTG AGC GGG AGC AAC GTG CTG GAG ACG GCC GTC ATC CTC						465
Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala Val Ile Leu						
85	90	95				
CTG CTG GAG GCC GGT GCA CTG GTG GCC CGG GCT GCG GTG CTG CAG CAG						513
Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln						

100	105	110	115	
CTG GAC AAT GTC ATT GAC GTG ATC ACC TGC AGC TCC ATG CTG TCC AGC Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser				561
120		125	130	
CTC TGC TTC CTG GGC GCC ATC GCC GTG GAC CGC TAC ATC TCC ATC TTC Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe				609
135		140	145	
TAC GCA CTG CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CGG CGA Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Arg Arg				657
150		155	160	
CGC GTT GCG GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC Arg Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe				705
165		170	175	
ATC GCC TAC TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe				753
180		185	190	195
TTC CTG GCT ATG CTG GTG CTC ATG GCC GTG CTG TAC GTC CAC ATG CTG Phe Leu Ala Met Leu Val Met Ala Val Leu Tyr Val His Met Leu				801
200		205	210	
GCC CGG GCC TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg				849
215		220	225	
CAG CGC CCG GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu				897
230		235	240	
ACC ATC CTG CTG GGC ATT TTC TTC CTC TGC TGG GGC CCC TTC TTC CTG Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu				945
245		250	255	
CAT CTC ACA CTC ATC GTC CTC TGC CCC GAG CAC CCC ACG TGC GGC TGC His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys				993
260		265	270	275
ATC TTC AAG AAC TTC AAC CTC TTT CTC GCC CTC ATC ATC TGC AAT GCC Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala				1041
280		285	290	
ATC ATC GAC CCC CTC ATC TAC GCC TTC CAC AGC CAG GAG CTC CGC AGG Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg				1089
295		300	305	
ACG CTC AAG GAG GTG CTG ACA TGC TCC TGG TGAGCGCGGT GCACGCGCTT Thr Leu Lys Glu Val Leu Thr Cys Ser Trp				1139
310		315		
TAAGTGTGCT GGGCAGAGGG AGGTGGTGAT ATTGTGTGGT CTGGTTCCCTG TGTGACCCCTG GGCAGTTCCCTG TACCTCCCTG GTCCCCGTTT GTCAAAGAGG ATGGACTAAA TGATCTCTGA				1199
				1259

AAGTGTTGAA G

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Val	Gln	Gly	Ser	Gln	Arg	Arg	Leu	Leu	Gly	Ser	Leu	Asn	Ser
1				5					10					15	
Thr	Pro	Thr	Ala	Ile	Pro	Gln	Leu	Gly	Leu	Ala	Ala	Asn	Gln	Thr	Gly
				20				25					30		
Ala	Arg	Cys	Leu	Glu	Val	Ser	Ile	Ser	Asp	Gly	Leu	Phe	Leu	Ser	Leu
				35				40				45			
Gly	Leu	Val	Ser	Leu	Val	Glu	Asn	Ala	Leu	Val	Val	Ala	Thr	Ile	Ala
				50				55			60				
Lys	Asn	Arg	Asn	Leu	His	Ser	Pro	Met	Tyr	Cys	Phe	Ile	Cys	Cys	Leu
				65				70		75			80		
Ala	Leu	Ser	Asp	Leu	Leu	Val	Ser	Gly	Ser	Asn	Val	Leu	Glu	Thr	Ala
				85				90				95			
Val	Ile	Leu	Leu	Leu	Glu	Ala	Leu	Val	Ala	Arg	Ala	Ala	Val		
				100				105			110				
Leu	Gln	Gln	Leu	Asp	Asn	Val	Ile	Asp	Val	Ile	Thr	Cys	Ser	Ser	Met
				115				120			125				
Leu	Ser	Ser	Leu	Cys	Phe	Leu	Gly	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Ile
				130				135			140				
Ser	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Val	Thr	Leu	Pro	Arg
				145				150		155			160		
Ala	Arg	Arg	Arg	Val	Ala	Ala	Ile	Trp	Val	Ala	Ser	Val	Val	Phe	Ser
				165				170			175				
Thr	Leu	Phe	Ile	Ala	Tyr	Tyr	Asp	His	Val	Ala	Val	Leu	Leu	Cys	Leu
				180				185			190				
Val	Val	Phe	Phe	Leu	Ala	Met	Leu	Val	Leu	Met	Ala	Val	Leu	Tyr	Val
				195				200			205				
His	Met	Leu	Ala	Arg	Ala	Cys	Gln	His	Ala	Gln	Gly	Ile	Ala	Arg	Leu
				210				215			220				
His	Lys	Arg	Gln	Arg	Pro	Val	His	Gln	Gly	Phe	Gly	Leu	Lys	Gly	Ala
				225				230		235			240		

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255

Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270

Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285

Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300

Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
 310 315

305

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGAATTCTG TGTGTNATCN CNGTGGACCG GTA

33

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGGATCCGA AGAAGGGAA CCAGCAGAGN ATGAA

35

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (PCR-fragment)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 1..285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTC TAC GCA CTG CGC TAC CAC AGC ATC GTG ACC ATG CGC CGC ACT GTG Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Met Arg Arg Thr Val 1 5 10 15	48
GTG GTG CTT ACG GTC ATC TGG ACG TTC TGC ACG GGG ACT GGC ATC ACC Val Val Leu Thr Val Ile Trp Thr Phe Cys Thr Gly Thr Gly Ile Thr 20 25 30	96
ATG GTG ATC TTC TCC CAT CAT GTG CCC ACA GTG ATC ACC TTC ACG TCG Met Val Ile Phe Ser His His Val Pro Thr Val Ile Thr Phe Thr Ser 35 40 45	144
CTG TTC CCG CTG ATG CTG GTC TTC ATC CTG TGC CTC TAT GTG CAC ATG Leu Phe Pro Leu Met Leu Val Phe Ile Leu Cys Leu Tyr Val His Met 50 55 60	192
TTC CTG CTG GCT CGA TCC CAC ACC AGG AAG ATC TCC ACC CTC CCC AGA Phe Leu Leu Ala Arg Ser His Thr Arg Lys Ile Ser Thr Leu Pro Arg 65 70 75 80	240
GCC AAC ATG AAA GGG GCC ATC ACC CTC ACC ATC CTG CTG GGC ATT Ala Asn Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Leu Gly Ile 85 90 95	285

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Met Arg Arg Thr Val 1 5 10 15	
Val Val Leu Thr Val Ile Trp Thr Phe Cys Thr Gly Thr Gly Ile Thr 20 25 30	
Met Val Ile Phe Ser His His Val Pro Thr Val Ile Thr Phe Thr Ser 35 40 45	
Leu Phe Pro Leu Met Leu Val Phe Ile Leu Cys Leu Tyr Val His Met 50 55 60	
Phe Leu Leu Ala Arg Ser His Thr Arg Lys Ile Ser Thr Leu Pro Arg 65 70 75 80	
Ala Asn Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Leu Gly Ile 85 90 95	

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (PCR-fragment)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..306
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:

TTC TAC GCA CTG CGC TAC CAC AGC ATC GTG ACG GCG AGG CGC TCA GGG Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Ala Arg Arg Ser Gly	48
1 5 10 15	
 GCC ATC ATC GCC GGC ATC TGG GCT TTC TGC ACG GGC TGC GGC ATT GTC Ala Ile Ile Ala Gly Ile Trp Ala Phe Cys Thr Gly Cys Gly Ile Val	96
20 25 30	
 TTC ATC CTG TAC TCA GAA TCC ACC TAC GTC ATC CTG TGC CTC ATC TCC Phe Ile Leu Tyr Ser Glu Ser Thr Tyr Val Ile Leu Cys Leu Ile Ser	144
35 40 45	
 ATG TTC TTC GCT ATG CTG TTC CTC CTG GTG TCT CTG TAC ATA CAC ATG Met Phe Phe Ala Met Leu Phe Leu Leu Val Ser Leu Tyr Ile His Met	192
50 55 60	
 TTC CTC CTG GCG CGG ACT CAC GTC AAG CGG ATC GCG CTC TGC CCG GGG Phe Leu Leu Ala Arg Thr His Val Lys Arg Ile Ala Leu Cys Pro Gly	240
65 70 75 80	
 CCA GCT CTG CGC GGC AGA GGA CCA GCA TGC AGG GGC GCG GTC ACC CTC Pro Ala Leu Arg Gly Arg Gly Pro Ala Cys Arg Gly Ala Val Thr Leu	288
85 90 95	
 ACC ATC CTG CTG GGC ATT Thr Ile Leu Leu Gly Ile	306
100	

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Ala Arg Arg Ser Gly
 1 5 10 15

Ala Ile Ile Ala Gly Ile Trp Ala Phe Cys Thr Gly Cys Gly Ile Val
 20 25 30

Phe Ile Leu Tyr Ser Glu Ser Thr Tyr Val Ile Leu Cys Leu Ile Ser
 35 40 45

Met Phe Phe Ala Met Leu Phe Leu Leu Val Ser Leu Tyr Ile His Met
 50 55 60

Phe Leu Leu Ala Arg Thr His Val Lys Arg Ile Ala Leu Cys Pro Gly
 65 70 75 80

Pro Ala Leu Arg Gly Arg Gly Pro Ala Cys Arg Gly Ala Val Thr Leu
 85 90 95

Thr Ile Leu Leu Gly Ile
 100

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (PCR-fragment)
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..312

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTC TAC GCA CTG CGT TAC CAC AGC ATC GTG ACC GTG CGG CGG GCC CTC Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Val Arg Arg Ala Leu	1 5 10 15	48
ACC TTG ATC GTG GCC ATC TGG GTC TGC TGC GGC GTC TGT GGC GTG GTG Thr Leu Ile Val Ala Ile Trp Val Cys Cys Gly Val Cys Gly Val Val	20 25 30	96
TTC ATC GTC TAC TCG GAG AGC AAA ATG GTC ATT GTG TGC CTC ATC ACC Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu Ile Thr	35 40 45	144
ATG TTC TTC GCC ATG ATG CTC CTC ATG GGC ACC CTC TAC GTG CAC ATG Met Phe Phe Ala Met Met Leu Leu Met Gly Thr Leu Tyr Val His Met	50 55 60	192
TTC CTC TTT GCG CGG CTG CAC GTC AAG CGC ATA GCA GCA CTG CCA CCT Phe Leu Phe Ala Arg Leu His Val Lys Arg Ile Ala Ala Leu Pro Pro	65 70 75 80	240
GCC GAC GGG GTG GCC CCA CAG CAA CAC TCA TGC ATG AAG GGG GCA GTC Ala Asp Gly Val Ala Pro Gln Gln His Ser Cys Met Lys Gly Ala Val	85 90 95	288

ACC CTC ACC ATC CTG CTG GGC ATT
 Thr Leu Thr Ile Leu Leu Gly Ile
 100

312

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: polypeptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Val Arg Arg Ala Leu
 1 5 10 15

Thr Leu Ile Val Ala Ile Trp Val Cys Cys Gly Val Cys Gly Val Val
 20 25 30

Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu Ile Thr
 35 40 45

Met Phe Phe Ala Met Met Leu Leu Met Gly Thr Leu Tyr Val His Met
 50 55 60

Phe Leu Phe Ala Arg Leu His Val Lys Arg Ile Ala Ala Leu Pro Pro
 65 70 75 80

Ala Asp Gly Val Ala Pro Gln Gln His Ser Cys Met Lys Gly Ala Val
 85 90 95

Thr Leu Thr Ile Leu Leu Gly Ile
 100

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (PCR-fragment)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..372

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTG TGT GTG ATC GCG CTG GAC CGG TAC ATC TCC ATC TTC TAC GCA CTG
 Leu Cys Val Ile Ala Leu Asp Arg Tyr Ile Ser Ile Phe Tyr Ala Leu
 1 5 10 15

48

CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CCG GAA GCC GTT GCG Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Pro Glu Ala Val Ala 20 25 30	96
GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC ATC GCC TAC Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile Ala Tyr 35 40 45	144
TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC TTC CTG GCT Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe Leu Ala 50 55 60	192
ATG CTG GTG CTC ATG GCC GTG CTG TAC GTC CAC ATG CTG GCC CGG GCC Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg Ala 65 70 75 80	240
TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG CAG CGC CCG Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln Arg Pro 85 90 95	288
GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC ACC ATC CTG Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr Ile Leu 100 105 110	336
CTG GGC ATT TTC ACC GTC TCG TGG CGC CCC TTC TAC Leu Gly Ile Phe Thr Val Ser Trp Arg Pro Phe Phe 115 120	372

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Cys Val Ile Ala Leu Asp Arg Tyr Ile Ser Ile Phe Tyr Ala Leu 1 5 10 15	
Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Pro Glu Ala Val Ala 20 25 30	
Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile Ala Tyr 35 40 45	
Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe Leu Ala 50 55 60	
Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg Ala 65 70 75 80	
Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln Arg Pro 85 90 95	

Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr Ile Leu
 100 105 110

Leu Gly Ile Phe Thr Val Ser Trp Arg Pro Phe Phe
 115 120

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGGAATTCTA CGCACTGCGC TACCACAGCA TCGTG

35

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGGGATCCAA TGCCCAGCAG GATGGTGAGG GTGA

34

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 616..1590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTTGAGGAGA ATGTCGTGCA GTAGCCTTAG GAATGTGAAC ATTGGGAGAC TGGCTGGGAT

60

TTTGTAGGTT ATGAGAAGGG GACACTTATG ATATGTGAAC TTGAGGCCAG GAGAGAAGCC

120

ATAAAAAGTG AAACTGTCTT GGGCACTTGG AGGTGAGTGT CTCTCTAGTA AGATGCATGT

180

GAAAGGCCTG GGAGCTGAAA GCAAGGAGAG CAGAAGAGGC TGGTGAAGAT TCTAATCTGC	240
GTGTCCAGGG GCACTCTTCC AGGTCTCAGG AACGCAGGTC AGAATGTGCA AGCCAGCTGC	300
CGGGCACGTG GCTCACCCCT GTAGTACCAAG CACTTTGGGA GGCTGAGAGA GAAGATCGCT	360
TGTGCCAGG AGTTTGAGAC CAGACTGGGG CTTCATAGGG AGACCCTGTC TCTTAAAAAA	420
AAAAAAAAAA AAGGACTGAG TGAGCCGAGC CCAGTCCTCT CATGCACTGT GTCATTCATC	480
CCCTTTCTTA GGCTGTGTTG GTTCTAGGCT AGCTGCTGTC TTTCTTGTT AGGCTGCTAA	540
CCTCTTGGA TTGTGAATTT AAAACATGTT TTACAGTAAA TTTGCTGCCA AGACAAGAGG	600
TGTATTTCTC CAGCA ATG AAT TCC TCA TTT CAC CTG CAT TTC TTG GAT CTC	651
Met Asn Ser Ser Phe His Leu His Phe Leu Asp Leu	
1 5 10	
AAC CTG AAT GCC ACA GAG GGU AAC CTT TCA GGA CCC AAT GTC AAA AAC	659
Asn Leu Asn Ala Thr Glu Gly Asn Leu Ser Gly Pro Asn Val Lys Asn	
15 20 25	
AAG TCT TCA CCA TGT GAA GAC ATG GGC ATT GCT GTG GAG GTG TTT CTC	747
Lys Ser Ser Pro Cys Glu Asp Met Gly Ile Ala Val Glu Val Phe Leu	
30 35 40	
ACT CTG GGT GTC ATC AGC CTC TTG GAG AAC ATC TTG GTC ATA GGG GCC	755
Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu Val Ile Gly Ala	
45 50 55 60	
ATA GTG AAG AAC AAA AAC CTG CAC TCC CCC ATG TAC TTC TTC GTG TGC	843
Ile Val Lys Asn Lys Asn Leu His Ser Pro Met Tyr Phe Phe Val Cys	
65 70 75	
AGC CTG GCA GTG GCG GAC ATG CTG GTG AGC ATG TCC AGT GCC TGG GAG	891
Ser Leu Ala Val Ala Asp Met Leu Val Ser Met Ser Ser Ala Trp Glu	
80 85 90	
ACC ATC ACC ATC TAC CTA CTC AAC AAC AAG CAC CTA GTG ATA GCA GAC	939
Thr Ile Thr Ile Tyr Leu Leu Asn Asn Lys His Leu Val Ile Ala Asp	
95 100 105	
GCC TTT GTG CGC CAC ATT GAC AAT GTG TTT GAC TCC ATG ATC TGC ATT	987
Ala Phe Val Arg His Ile Asp Asn Val Phe Asp Ser Met Ile Cys Ile	
110 115 120	
TCC GTG GTG GCA TCC ATG TGC AGC TTA CTG GCC ATT GCA GTG GAT AGG	1035
Ser Val Val Ala Ser Met Cys Ser Leu Leu Ala Ile Ala Val Asp Arg	
125 130 135 140	
TAC GTC ACC ATC TTC TAC GCC CTG CGC TAC CAC CAC ATC ATG ACG GCG	1083
Tyr Val Thr Ile Phe Tyr Ala Leu Arg Tyr His His Ile Met Thr Ala	
145 150 155	
AGG CGC TCA GGG GCC ATC ATC GCC GGC ATC TGG GCT TTC TGC ACG GGC	1131
Arg Arg Ser Gly Ala Ile Ile Ala Gly Ile Trp Ala Phe Cys Thr Gly	
160 165 170	

TGC GGC ATT GTC TTC ATC CTG TAC TCA GAA TCC ACC TAC GTC ATC CTG Cys Gly Ile Val Phe Ile Leu Tyr Ser Glu Ser Thr Tyr Val Ile Leu 175 180 185	1179
TGC CTC ATC TCC ATG TTC TTC GCT ATG CTG TTC CTC CTG GTG TCT CTG Cys Leu Ile Ser Met Phe Phe Ala Met Leu Phe Leu Leu Val Ser Leu 190 195 200	1227
TAC ATA CAC ATG TTC CTC CTG GCG CGG ACT CAC GTC AAG CGG ATC GCG Tyr Ile His Met Phe Leu Leu Ala Arg Thr His Val Lys Arg Ile Ala 205 210 215 220	1275
CTC TGC CCG GGG CCA GCT CTG CGC GGC AGA GGA CCA GCA TGG CAG GGC Leu Cys Pro Gly Pro Ala Leu Arg Gly Arg Gly Pro Ala Trp Gln Gly 225 230 235	1323
GCG GTC ACC GTC ACC ATG CTG CTG GGC GTG TTT ACC GTG TGC TGG GCC Ala Val Thr Val Thr Met Leu Leu Gly Val Phe Thr Val Cys Trp Ala 240 245 250	1371
CCG TTC CTT CAT CTC ACT TTA ATG CTT TCT TGC CCT CAG AAC CTC Pro Phe Phe Leu His Leu Thr Leu Met Leu Ser Cys Pro Gln Asn Leu 255 260 265	1419
TAC TGC TCT CGC TTC ATG TCT CAC TTC AAT ATG TAG CTC ATA CTC ATC Tyr Cys Ser Arg Phe Met Ser His Phe Asn Met Tyr Leu Ile Leu Ile 270 275 280	1467
ATG TGT AAT TCC GTG ATG GAC CCT CTC ATA TAT GCC TTC CGC AGC CAA Met Cys Asn Ser Val Met Asp Pro Leu Ile Tyr Ala Phe Arg Ser Gln 285 290 295 300	1515
GAG ATG CGG AAG ACC TTT AAG GAG ATT ATT TGC TGC CGT GGT TTC AGG Glu Met Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Arg Gly Phe Arg 305 310 315	1563
ATC GCC TGC AGC TTT CCC AGA AGG GAT TAACGACAAA GTGCTCCTCT Ile Ala Cys Ser Phe Pro Arg Arg Asp 320 325	1610
CTGTGGCTCT GTTCTCCTTT GTTTGCTCAC CTATGACAAA	1650

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Asn Ser Ser Phe His Leu His Phe Leu Asp Leu Asn Leu Asn Ala 1 5 10 15
Thr Glu Gly Asn Leu Ser Gly Pro Asn Val Lys Asn Lys Ser Ser Pro

20	25	30
Cys	Glu	Asp
35	35	40
Met	Gly	Ile
	Ala	Val
	Glu	Val
	Phe	Leu
	Thr	Leu
	Gly	Val
	45	
Ile	Ser	Leu
50	Leu	Glu
	Asn	Ile
	Leu	Val
	Ile	Gly
	Ala	Ile
	Val	Lys
	Asn	
Lys	Asn	Leu
65	His	Ser
	Pro	Met
	Tyr	Phe
	Phe	Val
	Cys	Ser
	Leu	Ala
	Val	
	80	
Ala	Asp	Met
	Leu	Val
	Ser	Met
	Ser	Ser
	Ala	Trp
	Glu	Thr
	Ile	Thr
	85	90
	95	
Tyr	Leu	Leu
100	Asn	Asn
	Lys	His
	Leu	Val
	Ile	Ala
	Asp	Ala
	Phe	Val
	Arg	
	105	110
His	Ile	Asp
115	Asn	Val
	Phe	Asp
	Ser	Met
	Ile	Cys
	Ile	Ser
	Val	Val
	Ala	
	120	125
Ser	Met	Cys
130	Ser	Leu
	Leu	Ala
	Ile	Ile
	Ala	Val
	Asp	Arg
	Tyr	Val
	Thr	Ile
	135	140
Phe	Tyr	Ala
145	Leu	Arg
	Tyr	His
	His	Ile
	Met	Thr
	Ala	Arg
	Arg	Ser
	Gly	
	150	155
	160	
Ala	Ile	Ile
165	Ala	Gly
	Ile	Trp
	Ala	Phe
	Cys	Thr
	Gly	Cys
	Ile	Val
	170	175
Phe	Ile	Leu
180	Tyr	Ser
	Glu	Ser
	Thr	Tyr
	Val	Ile
	Leu	Cys
	Ile	Ser
	185	190
Met	Phe	Phe
195	Ala	Met
	Leu	Phe
	Leu	Leu
	Val	Ser
	Leu	Tyr
	Tyr	Ile
	Ile	His
	195	200
	205	
Phe	Leu	Leu
210	Ala	Arg
	Thr	His
	Val	Val
	Lys	Arg
	Ile	Ala
	Leu	Cys
	Pro	Pro
	Gly	Gly
	215	220
	220	
Pro	Ala	Leu
225	Arg	Gly
	Arg	Gly
	Pro	Ala
	Trp	Gln
	Gly	Ala
	Ala	Val
	Thr	Val
	230	235
	240	
Thr	Met	Leu
	Leu	Gly
	Val	Phe
	Phe	Thr
	Val	Cys
	Cys	Trp
	Ala	Pro
	Pro	Phe
	Phe	Leu
	245	250
	255	
His	Leu	Thr
260	Leu	Met
	Met	Leu
	Leu	Ser
	Cys	Pro
	Pro	Gln
	Gln	Asn
	Asn	Leu
	Leu	Tyr
	Tyr	Cys
	Cys	Ser
	Ser	Arg
	265	270
	270	
Phe	Met	Ser
275	His	Phe
	Asn	Met
	Tyr	Leu
	Ile	Leu
	Ile	Met
	Met	Cys
	Cys	Asn
	Asn	Ser
	280	285
	285	
Val	Met	Asp
290	Pro	Leu
	Ile	Tyr
	Ala	Phe
	Phe	Arg
	Ser	Gln
	Gln	Glu
	Glu	Met
	Met	Arg
	Arg	Lys
	295	300
	300	
Thr	Phe	Lys
305	Glu	Ile
	Ile	Cys
	Cys	Arg
	Arg	Gly
	Gly	Phe
	Phe	Arg
	Arg	Ile
	Ile	Ala
	Ala	Cys
	Cys	Ser
	310	315
	320	
Phe	Pro	Arg
325	Arg	Asp

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO 17:

GGAAGCTTTC TTTGGTAGGC TG

22

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GGTCTAGAGC CACAGAGAGG AG

22

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CTGCATTTCT TGGATCT

17

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AAGCTGCACA TGGATGC

17